

GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: July 17, 2006, 09:45:23 ; Search time 118 Seconds  
(without alignments)  
4440.424 Million cell updates/sec

Title: US-10-791-844-1  
Perfect score: 5953  
Sequence: 1 MTRSPPLRELPPSYTPPART.....SPEILSPPAPQGGGLRPEEI 1146

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB ID	
1	5953	100.0	1146	3	AAY92225	Aay92225 Human pat
2	5932	99.6	1203	3	AAY92703	Aay92703 Human pat
3	5911	99.3	1203	2	AAY43261	Aay43261 Human pat
4	5911	99.3	1203	5	AAE19829	Aae19829 Human pat
5	5911	99.3	1203	6	ABG74104	Abg74104 Human pat
6	5909	99.3	1203	2	AAY28444	Aay28444 Human ptc
7	5420	91.0	1182	5	AAE19831	Aae19831 Mouse pat
8	3326.5	55.9	1447	2	AAR75375	Aar75375 Human pat
9	3326.5	55.9	1447	2	AAW52200	Aaw52200 Human pat
10	3326.5	55.9	1447	2	AAW72969	Aaw72969 Human pat
11	3326.5	55.9	1447	4	AAB67163	Aab67163 Human pat
12	3326.5	55.9	1447	5	AAE19830	Aae19830 Human pat
13	3326.5	55.9	1447	5	ABJ10931	Abj10931 TRC8 rela
14	3326.5	55.9	1447	5	AAG79571	Aag79571 Human pat
15	3326.5	55.9	1447	7	ABU62275	Abu62275 Human pat
16	3326.5	55.9	1447	7	ADD46678	Add46678 Human Pro

17	3326.5	55.9	1447	7	ADE94224	Ade94224 Human ptc
18	3326.5	55.9	1447	7	ADH62731	Adh62731 Human pat
19	3326.5	55.9	1447	8	ADE48989	Ade48989 Human pat
20	3326.5	55.9	1447	9	AEC94931	Aec94931 Human pat
21	3315.5	55.7	1434	2	AAW52199	Aaw52199 Mouse pat
22	3315.5	55.7	1434	2	AAW72968	Aaw72968 Mouse pat
23	3315.5	55.7	1434	4	AAB67159	Aab67159 Murine pa
24	3315.5	55.7	1434	5	AAG79572	Aag79572 Mouse pat
25	3315.5	55.7	1434	7	ABU62271	Abu62271 Mouse pat
26	3315.5	55.7	1434	7	ADE94215	Ade94215 Murine pt
27	3315.5	55.7	1434	7	ADH62722	Adh62722 Mouse pat
28	3315.5	55.7	1434	8	ADE48980	Ade48980 Mouse pat
29	3315.5	55.7	1434	9	AEC94922	Aec94922 Mouse pat
30	3313.5	55.7	1434	2	AAR94380	Aar94380 Mouse pat
31	3024.5	50.8	1296	2	AAW47157	Aaw47157 Nevoid ba
32	2613	43.9	529	2	AAW82586	Aaw82586 Human Pat
33	2220	37.3	1311	2	AAW52197	Aaw52197 Precis co
34	2219	37.3	1311	2	AAW72971	Aaw72971 Precis co
35	2219	37.3	1311	4	AAB67156	Aab67156 Butterfly
36	2219	37.3	1311	5	AAG79573	Aag79573 Butterfly
37	2219	37.3	1311	7	ABU62149	Abu62149 Buckeye p
38	2219	37.3	1311	7	ADE94209	Ade94209 Peacock b
39	2219	37.3	1311	7	ADH62716	Adh62716 Butterfly
40	2219	37.3	1311	8	ADE48974	Ade48974 Butterfly
41	2219	37.3	1311	9	AEC94916	Aec94916 Butterfly
42	2212	37.2	1318	9	AEC94977	Aec94977 Butterfly
43	1981	33.3	1286	4	ABB59092	Abb59092 Drosophil
44	1981	33.3	1286	5	ABJ10929	Abj10929 TRC8 rela
45	1950.5	32.8	1299	2	AAR86304	Aar86304 Drosophil

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OM protein - protein search, using sw model

Run on: July 17, 2006, 09:48:33 ; Search time 34 Seconds  
 (without alignments)  
 2950.297 Million cell updates/sec

Title: US-10-791-844-1  
 Perfect score: 5953  
 Sequence: 1 MTRSPPLRELPPSYTPPART.....SPEILSPPAPQGGGLRPEEI 1146

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_AA:  
 1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:  
 2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:  
 3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:  
 4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:  
 5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCTUS\_COMB.pep:  
 6: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:  
 7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	5953	100.0	1146	2	US-09-807-007-1	Sequence 1, Appli
2	5911	99.3	1203	2	US-09-293-505-2	Sequence 2, Appli
3	5911	99.3	1203	2	US-09-060-939A-2	Sequence 2, Appli
4	5909	99.3	1203	2	US-09-207-857-2	Sequence 2, Appli
5	5909	99.3	1203	2	US-09-909-280A-2	Sequence 2, Appli
6	5420	91.0	1182	2	US-09-293-505-7	Sequence 7, Appli
7	5420	91.0	1182	2	US-09-060-939A-7	Sequence 7, Appli
8	3326.5	55.9	1447	1	US-08-540-406-19	Sequence 19, Appli
9	3326.5	55.9	1447	2	US-08-656-055-19	Sequence 19, Appli
10	3326.5	55.9	1447	2	US-08-954-668-19	Sequence 19, Appli
11	3326.5	55.9	1447	2	US-09-268-140-5	Sequence 5, Appli
12	3326.5	55.9	1447	2	US-08-918-658-19	Sequence 19, Appli
13	3326.5	55.9	1447	2	US-09-724-631-19	Sequence 19, Appli
14	3326.5	55.9	1447	2	US-08-954-701A-19	Sequence 19, Appli
15	3326.5	55.9	1447	2	US-09-807-007-6	Sequence 6, Appli
16	3326.5	55.9	1447	2	US-09-754-032-19	Sequence 19, Appli
17	3326.5	55.9	1447	2	US-08-916-140-19	Sequence 19, Appli
18	3326.5	55.9	1447	5	PCT-US95-13233-19	Sequence 19, Appli
19	3315.5	55.7	1434	1	US-08-540-406-10	Sequence 10, Appli

20	3315.5	55.7	1434	2	US-08-656-055-10	Sequence 10, Appl
21	3315.5	55.7	1434	2	US-08-954-668-10	Sequence 10, Appl
22	3315.5	55.7	1434	2	US-08-918-658-10	Sequence 10, Appl
23	3315.5	55.7	1434	2	US-09-724-631-10	Sequence 10, Appl
24	3315.5	55.7	1434	2	US-08-954-701A-10	Sequence 10, Appl
25	3315.5	55.7	1434	2	US-09-754-032-10	Sequence 10, Appl
26	3315.5	55.7	1434	2	US-08-916-140-10	Sequence 10, Appl
27	3315.5	55.7	1434	5	PCT-US95-13233-10	Sequence 10, Appl
28	3024.5	50.8	1296	2	US-08-857-636-60	Sequence 60, Appl
29	2613	43.9	529	2	US-09-500-063-2	Sequence 2, Appli
30	2219	37.3	1311	1	US-08-540-406-4	Sequence 4, Appli
31	2219	37.3	1311	2	US-08-656-055-4	Sequence 4, Appli
32	2219	37.3	1311	2	US-08-954-668-4	Sequence 4, Appli
33	2219	37.3	1311	2	US-08-918-658-4	Sequence 4, Appli
34	2219	37.3	1311	2	US-09-724-631-4	Sequence 4, Appli
35	2219	37.3	1311	2	US-08-954-701A-4	Sequence 4, Appli
36	2219	37.3	1311	2	US-09-754-032-4	Sequence 4, Appli
37	2219	37.3	1311	2	US-08-916-140-4	Sequence 4, Appli
38	2219	37.3	1311	5	PCT-US95-13233-4	Sequence 4, Appli
39	1981	33.3	1286	2	US-09-268-140-3	Sequence 3, Appli
40	1950.5	32.8	1299	2	US-08-460-900C-62	Sequence 62, Appl
41	1950.5	32.8	1299	2	US-08-674-509B-48	Sequence 48, Appl
42	1950.5	32.8	1299	2	US-08-954-698-48	Sequence 48, Appl
43	1950.5	32.8	1299	2	US-09-639-695-62	Sequence 62, Appl
44	1950.5	32.8	1299	2	US-09-448-188-48	Sequence 48, Appl
45	1950.5	32.8	1299	2	US-08-954-128-48	Sequence 48, Appl

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OM protein - protein search, using sw model

Run on: July 17, 2006, 09:48:44 ; Search time 110 Seconds  
(without alignments)  
4825.857 Million cell updates/sec

Title: US-10-791-844-1  
Perfect score: 5953  
Sequence: 1 MTRSPPLRELPPSYTPPART.....SPEILSPPAPQGGGLRPEEI 1146

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_Main:  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result No.	Query Score	Match	Length	DB	ID	Description
1	5953	100.0	1146	4	US-10-791-844-1	Sequence 1, Appli
2	5911	99.3	1203	3	US-09-990-046-2	Sequence 2, Appli
3	5909	99.3	1203	3	US-09-909-280A-2	Sequence 2, Appli
4	5420	91.0	1182	3	US-09-990-046-7	Sequence 7, Appli
5	3326.5	55.9	1447	2	US-08-954-701A-19	Sequence 19, Appli
6	3326.5	55.9	1447	3	US-09-898-533-5	Sequence 5, Appli
7	3326.5	55.9	1447	3	US-09-754-032-19	Sequence 19, Appli
8	3326.5	55.9	1447	4	US-10-421-446-19	Sequence 19, Appli
9	3326.5	55.9	1447	4	US-10-791-844-6	Sequence 6, Appli
10	3315.5	55.7	1434	2	US-08-954-701A-10	Sequence 10, Appli
11	3315.5	55.7	1434	3	US-09-754-032-10	Sequence 10, Appli
12	3315.5	55.7	1434	4	US-10-421-446-10	Sequence 10, Appli
13	3024.5	50.8	1296	4	US-10-302-279-60	Sequence 60, Appli
14	2219	37.3	1311	2	US-08-954-701A-4	Sequence 4, Appli
15	2219	37.3	1311	3	US-09-754-032-4	Sequence 4, Appli
16	2219	37.3	1311	4	US-10-421-446-4	Sequence 4, Appli
17	1981	33.3	1286	3	US-09-898-533-3	Sequence 3, Appli
18	1981	33.3	1286	6	US-11-097-143-4068	Sequence 4068, Ap
19	1950.5	32.8	1299	2	US-08-954-771-48	Sequence 48, Appli
20	1950.5	32.8	1299	5	US-10-647-654-48	Sequence 48, Appli

21	1950.5	32.8	1299	5	US-10-835-517-48	Sequence 48, Appli
22	1925.5	32.3	1285	2	US-08-954-701A-6	Sequence 6, Appli
23	1925.5	32.3	1285	3	US-09-754-032-6	Sequence 6, Appli
24	1925.5	32.3	1285	4	US-10-421-446-6	Sequence 6, Appli
25	1707	28.7	1405	4	US-10-369-493-5464	Sequence 5464, Ap
26	992	16.7	714	4	US-10-369-493-5410	Sequence 5410, Ap
27	642	10.8	1278	4	US-10-208-731-2	Sequence 2, Appli
28	642	10.8	1278	4	US-10-741-601-530	Sequence 530, App
29	642	10.8	1278	5	US-10-741-600-1542	Sequence 1542, Ap
30	642	10.8	1278	5	US-10-756-149-4924	Sequence 4924, Ap
31	642	10.8	1278	5	US-10-995-561-952	Sequence 952, App
32	604.5	10.2	1319	4	US-10-208-731-4	Sequence 4, Appli
33	596.5	10.0	1359	4	US-10-621-758A-44	Sequence 44, Appli
34	596.5	10.0	1359	4	US-10-663-208A-44	Sequence 44, Appli
35	596.5	10.0	1359	4	US-10-646-301A-44	Sequence 44, Appli
36	596.5	10.0	1359	4	US-10-736-769-44	Sequence 44, Appli
37	585	9.8	1332	4	US-10-239-316-9	Sequence 9, Appli
38	585	9.8	1332	6	US-11-242-459-9	Sequence 9, Appli
39	584.5	9.8	1331	4	US-10-621-758A-2	Sequence 2, Appli
40	584.5	9.8	1331	4	US-10-663-208A-2	Sequence 2, Appli
41	584.5	9.8	1331	4	US-10-646-301A-2	Sequence 2, Appli
42	584.5	9.8	1331	4	US-10-736-769-2	Sequence 2, Appli
43	579	9.7	1332	4	US-10-621-758A-4	Sequence 4, Appli
44	579	9.7	1332	4	US-10-663-208A-4	Sequence 4, Appli
45	579	9.7	1332	4	US-10-646-301A-4	Sequence 4, Appli

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OM protein - protein search, using sw model

Run on: July 17, 2006, 09:48:55 ; Search time 58 Seconds  
(without alignments)  
1130.354 Million cell updates/sec

Title: US-10-791-844-1  
Perfect score: 5953  
Sequence: 1 MTRSPPLRELPPSYTPPART.....SPEILSPPAPQGGGLRPEEI 1146

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 204771 seqs, 57208143 residues

Total number of hits satisfying chosen parameters: 204771

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published\_Applications\_AA\_New:  
1: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:  
2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:  
3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:  
4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:  
5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:  
6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:  
7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:  
8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result No.	Score	Query			Description
		Match	Length	DB ID	
1	596.5	10.0	1359	7 US-11-270-796-22	Sequence 22, Appl
2	548.5	9.2	1333	7 US-11-270-796-3	Sequence 3, Appli
3	478.5	8.0	1279	6 US-10-449-902-53619	Sequence 53619, A
4	361	6.1	419	6 US-10-953-349-21065	Sequence 21065, A
5	155	2.6	967	6 US-10-505-405-6	Sequence 6, Appli
6	150	2.5	967	6 US-10-505-405-2	Sequence 2, Appli
7	112	1.9	829	6 US-10-471-571A-3682	Sequence 3682, Ap
8	110	1.8	316	7 US-11-056-355B-12238	Sequence 12238, A
9	106.5	1.8	1089	6 US-10-196-749-266	Sequence 266, App
10	104	1.7	463	6 US-10-449-902-53826	Sequence 53826, A
11	103.5	1.7	675	6 US-10-449-902-41195	Sequence 41195, A
12	103	1.7	754	7 US-11-056-355B-69815	Sequence 69815, A
13	102.5	1.7	441	7 US-11-056-355B-5400	Sequence 5400, Ap
14	102	1.7	776	7 US-11-056-355B-69962	Sequence 69962, A
15	101.5	1.7	3696	7 US-11-330-363-4	Sequence 4, Appli
16	101	1.7	355	6 US-10-449-902-37525	Sequence 37525, A
17	101	1.7	355	6 US-10-449-902-44499	Sequence 44499, A
18	101	1.7	694	6 US-10-517-420-46	Sequence 46, Appl

19	100.5	1.7	272	6	US-10-953-349-27853	Sequence 27853, A
20	100.5	1.7	282	6	US-10-953-349-27852	Sequence 27852, A
21	100	1.7	632	7	US-11-293-697-3548	Sequence 3548, Ap
22	98	1.6	444	6	US-10-471-571A-2436	Sequence 2436, Ap
23	98	1.6	672	6	US-10-449-902-52633	Sequence 52633, A
24	97.5	1.6	586	6	US-10-505-405-8	Sequence 8, Appli
25	96.5	1.6	471	6	US-10-449-902-38281	Sequence 38281, A
26	96	1.6	443	6	US-10-449-902-40171	Sequence 40171, A
27	96	1.6	529	6	US-10-449-902-43353	Sequence 43353, A
28	96	1.6	715	6	US-10-449-902-53933	Sequence 53933, A
29	95.5	1.6	434	6	US-10-953-349-4711	Sequence 4711, Ap
30	95.5	1.6	434	7	US-11-056-355B-24988	Sequence 24988, A
31	95.5	1.6	507	6	US-10-953-349-4710	Sequence 4710, Ap
32	95.5	1.6	507	7	US-11-056-355B-24987	Sequence 24987, A
33	95.5	1.6	507	7	US-11-056-355B-27941	Sequence 27941, A
34	95.5	1.6	507	7	US-11-056-355B-31531	Sequence 31531, A
35	95.5	1.6	512	6	US-10-953-349-4709	Sequence 4709, Ap
36	95.5	1.6	512	7	US-11-056-355B-24986	Sequence 24986, A
37	95.5	1.6	512	7	US-11-056-355B-27940	Sequence 27940, A
38	95.5	1.6	512	7	US-11-056-355B-31530	Sequence 31530, A
39	95.5	1.6	539	7	US-11-056-355B-27939	Sequence 27939, A
40	95.5	1.6	539	7	US-11-056-355B-31529	Sequence 31529, A
41	95.5	1.6	699	6	US-10-196-749-138	Sequence 138, App
42	95	1.6	1333	6	US-10-449-902-41289	Sequence 41289, A
43	94.5	1.6	334	7	US-11-056-355B-19520	Sequence 19520, A
44	94.5	1.6	375	7	US-11-056-355B-19519	Sequence 19519, A
45	94.5	1.6	514	6	US-10-449-902-40710	Sequence 40710, A

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OM protein - protein search, using sw model

Run on: July 17, 2006, 09:47:43 ; Search time 28 Seconds  
 (without alignments)  
 3938.015 Million cell updates/sec

Title: US-10-791-844-1  
 Perfect score: 5953  
 Sequence: 1 MTRSPPLRELPPSYTPPART.....SPEILSPPAPQGGGLRPEEI 1146

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_80:\*

- 1: pirl:\*
- 2: pir2:\*
- 3: pir3:\*
- 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query	%				
No.	Score	Match	Length	DB	ID	Description
1	5420	91.0	1182	2	T13952	membrane protein p
2	4033.5	67.8	1220	2	T18291	patched protein -
3	3321.5	55.8	1442	2	T18538	patched protein -
4	3315.5	55.7	1434	2	T30172	transmembrane prot
5	1950.5	32.8	1299	1	S06119	membrane protein p
6	1707	28.7	1405	2	T27969	hypothetical prote
7	992	16.7	714	2	T16126	hypothetical prote
8	604.5	10.2	1278	2	T30188	Niemann-Pick C dis
9	511	8.6	1055	2	T05663	hypothetical prote
10	462	7.8	955	2	T21612	hypothetical prote
11	444	7.5	933	2	T25600	hypothetical prote
12	441	7.4	1003	2	T26746	hypothetical prote
13	433.5	7.3	1015	2	T15830	hypothetical prote
14	416.5	7.0	889	2	T29590	hypothetical prote
15	394	6.6	936	2	T26521	hypothetical prote
16	386.5	6.5	956	2	A89153	protein C24B5.3 [i]
17	383.5	6.4	1170	2	S52525	probable membrane
18	343	5.8	881	2	T31739	hypothetical prote
19	340.5	5.7	845	2	T25657	hypothetical prote
20	321.5	5.4	800	2	T26683	hypothetical prote
21	311	5.2	877	2	T24097	hypothetical prote
22	310	5.2	820	2	T32908	hypothetical prote

23	300.5	5.0	983	2	T21213	hypothetical prote
24	295.5	5.0	1456	2	T15961	hypothetical prote
25	292	4.9	840	2	T33217	hypothetical prote
26	272.5	4.6	871	2	T28706	hypothetical prote
27	268.5	4.5	890	2	T22186	hypothetical prote
28	261.5	4.4	690	2	T23399	hypothetical prote
29	192	3.2	1028	2	H71918	probable efflux tr
30	185	3.1	1276	2	T18526	SREBP cleavage act
31	184	3.1	1028	2	G64595	acriflavine resist
32	178	3.0	787	2	H71453	hypothetical prote
33	176.5	3.0	746	2	A75018	transport protein
34	172.5	2.9	633	2	S44795	F09G8.3 protein -
35	167.5	2.8	888	2	E71280	probable antibioti
36	164.5	2.8	1028	2	AD0052	probable multi-dru
37	164.5	2.8	1154	2	T48829	related to SREBP c
38	162	2.7	1077	2	H96007	probable acriflavi
39	160	2.7	932	2	T28820	hypothetical prote
40	157	2.6	1027	2	F82829	acriflavin resista
41	155	2.6	749	2	H91170	hypothetical membr
42	154	2.6	772	2	H86016	hypothetical prote
43	153	2.6	736	1	C69307	conserved hypothet
44	150	2.5	1053	2	D83206	probable RND efflu
45	149	2.5	1000	2	F70368	cation efflux (Acr

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OM protein - protein search, using sw model

Run on: July 17, 2006, 09:45:44 ; Search time 163 Seconds  
(without alignments)  
6503.484 Million cell updates/sec

Title: US-10-791-844-1  
Perfect score: 5953  
Sequence: 1 MTRSPPLRELPPSYTPPART.....SPEILSPPAPQGGGLRPEEI 1146

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

Result No.	Query Score	Match	Length	DB	ID	Description
<hr/>						
1	5919	99.4	1203	1	PTC2_HUMAN	Q9y6c5 homo sapien
2	5911	99.3	1203	2	Q53Z57_HUMAN	Q53z57 homo sapien
3	5420	91.0	1182	1	PTC2_MOUSE	O35595 mus musculu
4	4104	68.9	1413	2	Q9DEF3_XENLA	Q9def3 xenopus lae
5	4094	68.8	1422	2	Q6IRAS5_XENLA	Q6ira5 xenopus lae
6	4033.5	67.8	1220	1	PTC1_BRARE	Q98864 brachydanio
7	3374	56.7	1197	2	Q4RVD6_TETNG	Q4rvd6 tetraodon n
8	3338	56.1	913	2	Q90XB9_CHICK	Q90xb9 gallus gall
9	3326.5	55.9	1447	1	PTC1_HUMAN	Q13635 homo sapien
10	3324.5	55.8	1434	2	Q6UY90_RAT	Q6uy90 rattus norv
11	3321.5	55.8	1442	1	PTC1_CHICK	Q90693 gallus gall
12	3315.5	55.7	1434	1	PTC1_MOUSE	Q61115 mus musculu
13	3308.5	55.6	1434	2	Q2MHN4_MERUN	Q2mhn4 meriones un
14	3289	55.2	1239	2	Q9DEF4_XENLA	Q9def4 xenopus lae
15	3289	55.2	1418	2	Q98SW6_XENLA	Q98sw6 xenopus lae
16	3252	54.6	1243	2	Q9W6T6_BRARE	Q9w6t6 brachydanio
17	3030.5	50.9	1296	2	Q5VZC2_HUMAN	Q5vzc2 homo sapien
18	2226	37.4	1318	2	Q9XYP5_JUNCO	Q9xyp5 junonia coe
19	1993.5	33.5	1075	2	Q4T1E7_TETNG	Q4t1e7 tetraodon n
20	1981	33.3	1286	1	PTC_DROME	P18502 drosophila
21	1931.5	32.4	939	2	Q7Q2Y4_ANOGA	Q7q2y4 anopheles g
22	1798	30.2	651	2	Q6TKP9_HUMAN	Q6tkp9 homo sapien
23	1779.5	29.9	608	2	Q9Z2A1_RAT	Q9z2a1 rattus norv
24	1710	28.7	1402	2	Q61Z32_CAEBR	Q61z32 caenorhabdi

25	1707	28.7	1405	1	PTC1_CAEEL	Q09614 caenorhabdi
26	1646.5	27.7	1380	2	Q60VE7_CAEBR	Q60ve7 caenorhabdi
27	1631	27.4	1358	2	Q6AW15_CAEEL	Q6aw15 caenorhabdi
28	1629.5	27.4	1361	2	Q6AW16_CAEEL	Q6aw16 caenorhabdi
29	1556	26.1	586	2	Q59FG5_HUMAN	Q59fg5 homo sapien
30	1534	25.8	493	2	Q5EFR6_AMBME	Q5efr6 ambystoma m
31	1099	18.5	976	2	Q4H2Z6_CIOIN	Q4h2z6 ciona intes
32	992	16.7	667	2	Q09540_CAEEL	Q09540 caenorhabdi
33	984	16.5	255	1	PTC2_CYNPY	O42334 cynops pyrr
34	866.5	14.6	287	2	Q9DDZ0_XENLA	Q9ddz0 xenopus lae
35	866	14.5	348	2	Q3LFT4_HUMAN	Q3lft4 homo sapien
36	797	13.4	257	1	PTC1_CYNPY	O42335 cynops pyrr
37	790	13.3	247	2	Q3UUD4_MOUSE	Q3uud4 mus musculu
38	769	12.9	234	2	Q8MKB3_HORSE	Q8mkb3 equus cabal
39	765.5	12.9	259	2	Q5R2Z2_MOUSE	Q5r2z2 mus musculu
40	762.5	12.8	259	2	Q5R1V0_HUMAN	Q5r1v0 homo sapien
41	762.5	12.8	324	2	Q5R1U9_HUMAN	Q5r1u9 homo sapien
42	701	11.8	176	2	Q66PH3_ASTFA	Q66ph3 astyanax fa
43	642	10.8	1278	1	NPC1_HUMAN	O15118 homo sapien
44	642	10.8	1289	2	Q59GR1_HUMAN	Q59gr1 homo sapien
45	638	10.7	1277	1	NPC1_PIG	P56941 sus scrofa